

Fig. 1

h: 1 MSGSTQPVAQWTRATEPRYPH... ARHTHTDVGLLEYQHHSRDYASHLSPGSIQPORR... QPGNERSQELHLRPESHSYLPELGKSEM  
m: 1 -A-----GI-----S-----P-----T-----S-----RTF-----PDI

h: 101 EFIESKRPRLELLPDPLLRPSPLLATGQPAGEDLTkdRSLTGKLEPVSPSPPHTDPELELVPPRLSKEELIQN.MDRVDREITMVEQQISKKKKQQQ  
m: 101 -T-----T-----S-----A-----A-----A-S-----RL

h: 200 LEEAAKPPEPEKPVSPPIESKHRSVLQIIYDENRKKAAEAHRIEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWEQKFC  
m: 201 -----R-

h: 300 QRYDQLMEAWKVERIENNPRRRAKESKVREYKQFPEIRKQRELQERMQ.RVGQRGSGLSMSPARSEHEVSEIIDGLSEQENLEKQMRQLAVIPML  
m: 301 -----S-----A-----RHV

h: 399 YDADQQRIFKFINMGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVAECVLYLYLTKKKENYKSLVRRSYRRRGKSQQQQQQ  
m: 401 .RR-----D-----T-----RD-----

h: 499 QQQQQQQQQQPMPRSSQEEKDEKEKEKEAEKEEEKPEVENDKEDLLKEKTDTSGEDNDEKEAVASKGRKTANSQGRKGRITRSMANEANSEEAITPQ  
m: 500 -----A-----E-----D-----QDA-----E-----S-----H-----TA-----

h: 599 QSAELASMELNESSRWTEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQHKLMKERNARRKKKKAPAAASEEAAFPV  
m: 596 --S-----M-----T-----T-----A  
m: -AC: --S-----M-----HQTPGPGARLLTQQELRAPIPSTPQLQPHSHRPHPSKEPCTPPCQSGPAGHLGLRSAPRKDSK\*

h: 699 VEDEEMASGVGTGNEEMVEEAEAT.....VNNSDTEISIPSPHTEAAKDTGQNGPKPPATLGADGPPGPPPTPPEDIPAPTESTP  
m: 696 A-----SA-----LA-----SQASGNEVPRVGECSGPAA-----V-----RS-----T-----G-EALPAATQP-VP--E-PAA--A-PS-

h: 781 ASEATLAPTPPPAPPFPSPPPVPKKEEBETAAAPPVEEGEEKPPAAEELAVDTGKAEEP.....VKSECTEEAEAGPA.KGKDAEAAEATAE  
m: 793 VPD-SGPPS-E-S-S.-AA--AT-D-D-Q-APA-P--QT-DAK--SEAE...I-V--P--EASEEPES--DHK--T--E-ED-A-GT--I-TVS-

h: 871 RALKAKEGGSGRATTAKSSGAPQDSDSATCSADEVDEAEGGDKNRLSPRPSLLTPTGDPANASPOKPLDLKQLKQRAAAIPIQTVKHEPPRED  
m: 889 AP--V-.EAGSKAAV-KGS--T-----P-----G-----A-----ST-----

MEAWDAH-P->(SMRT)

h: 971 AAPT KPAPPAPPQNLQPESDAPQPGSSPRGKSRSPAPPADKEAEKPVFFPAFAAEQKLPDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPP  
m: 987 TV-P--V--V--T-H--G-VS--S-G-----V--E-----A-----PT-G-SYRLS-HA.GHR--SH-----T-TR--L--T--

h: 1071 GHPLPLGLHDTARPVLPRPTTISNPPLISSAKHPSVLERQIGAISQMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGP  
m: 1083 -----S-----G-----R--H-----M--L--E--AV-----GTALAPPPVEA--ASQ..

h: 1171 PESLGVPTAQEASVLRGTALGSVPGGSITKGIPTSTRVPSDSAITYRGSITHGTPADVLVKGITITRIIGEDSPSRDLRGREDSLPKGHVIEYEGKKGHVLSY  
m: 1179 -----Y-GC-R-QLQRLYH....PR-----S--V-----A--T-----

h: 1271 EGGMSVTQCKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHRGSITQGI PRSYVEAQEDYLRREAKLLKR  
m: 1243 -----S-----TVT-----Q-----

h: 1371 EGTPPPPPSRDLTEAYKTQ...ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKHVDVRSLI  
m: 1341 -----P-----T--PRPLDP-----T--V-----R-----S--PS--T-----

h: 1468 GSPGRTPFPVHPLDVMADARALERACYEESLKS RPTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSS  
m: 1441 -----P--AL-----I-----S--S-GA--T-----V-----TS-----T-----L-----

h: 1568 KASQDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLRGVSGVDLYRSHIPLAFDPTSIPRGIPLD.AAAAYLPRHLAPNPTYPHLYPPYLIRGYPD  
m: 1541 -----T-----G-----EA-----S-----

M->(TRAC1)

h: 1667 AALENQTIINDYITSQQMHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSP  
m: 1641 -----A-S-----S-----I-----P-----H-----

h: 1767 LSPGPGTHLTKPTTTSSSERERDRDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHPISPRTO DALQORPS  
m: 1741 -----A--A-----E-E-----G-----

h: 1867 VLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPFATHCPLGGTLDGVYPTLMPEVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPS  
m: 1825 -----S--V-S--GT-----E-----TS-----V-G--T-----

h: 1967 KGSEPRPLVPPVSGHATIARTPAKNLAPHASPDPPAPPASADPHREKTQSKPFSIQELELRSLGYH.GSSYSPEGVEPVSPVSSPSLTHDKGLPKHLE  
m: 1922 -S--S-A--S-S-TA-----S-----G--T--L-----S-AG--D--I-----S-P--

h: 2066 ELDKSHLEGLRPKQPQPGVKLGGEAAHLPHLRPLPESQSSSPLLTQAPGVKGHRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSPFGASCPVLD  
m: 2021 --E-----H-----M--SA-----I-----G-----

h: 2166 LRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSVAVYLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKL  
m: 2121 -----T-----S-----SS--A-----A-----G-----

h: 2266 TESNSAMVSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLM TYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPLSANAFNPLNAS  
m: 2220 -----G-----A-----C-----P--G-----

h: 2366 SLP.AAMPITAADGRSDHTLTSPGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAG  
m: 2320 ---A-----T-----A-----

h: 2465 VMASPPPPGLPAGSGPLAGPHAWDEEPKPLLC SQYETLSDSE 2507  
m: 2420 -----A-----2462

Fig. 2

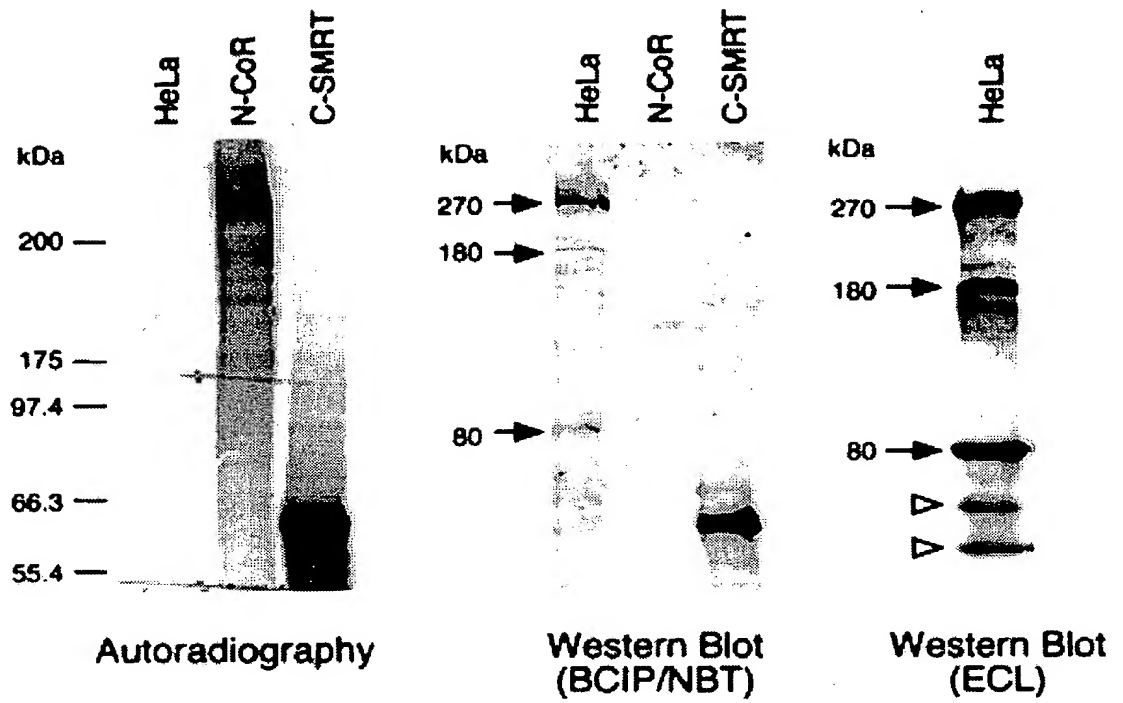


Fig. 3

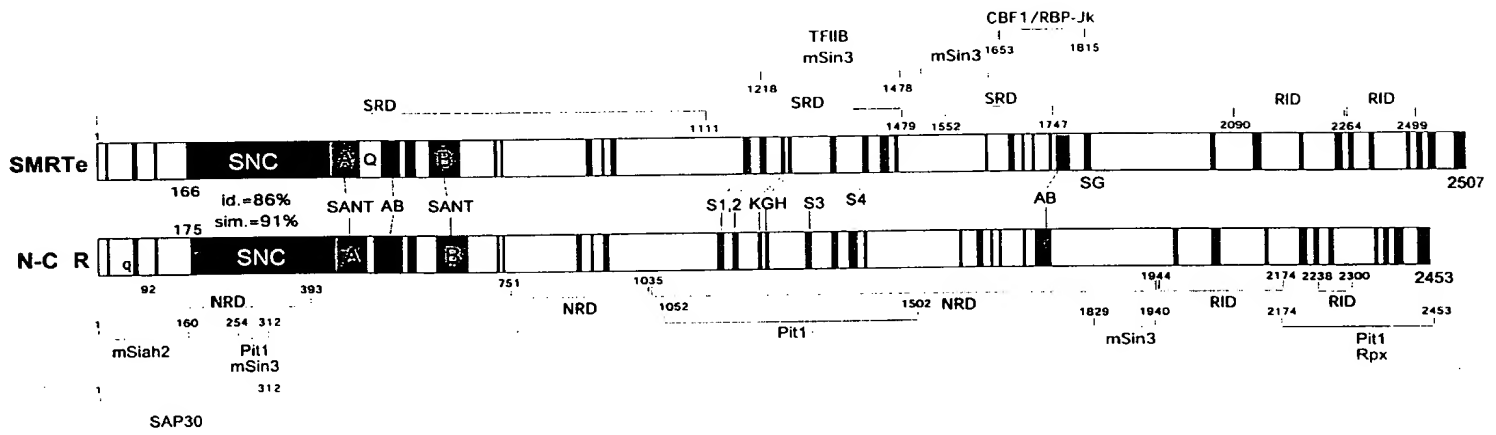


Fig. 4

hS 166 RLSKEELIQN.MDRVDREITMVEQQISKIKKKQQQLEEEAAKPPPEPEKPV  
mS 166 RLSKEELIQN.MDRVDREITMVEQQISKIKKKQQQLEEEAAKPPPEPEKPV  
hN 175 RLSKEELIQS.MDRVDREIAKVEQQILKIKKKQQQLEEEAAKPPPEPEKPV  
mN 175 RLSKEELIQS.MDRVDREIAKVEQQILKIKKKQQQLEEEAAKPPPEPEKPV

hS 215 SPPPIESKHRSIVQIIYDENRKKAEAAHRILEGLGPOVELPLYNQPSDTR  
mS 216 SPPPIESKHRSIVQIIYDENRKKAEAAHRILEGLGPOVELPLYNQPSDTR  
hN 224 SPPPIESKHRSIVQIIYDENRKKAEAAHRILEGLGPOVELPLYNQPSDTR  
mN 224 SPPPIESKHRSIVQIIYDENRKKAEAAHRILEGLGPOVELPLYNQPSDTR

hS 265 QYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEMEAWKKVE  
mS 266 QYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEMEAWKKVE  
hN 274 VYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEMEAWKKVE  
mN 274 VYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEMEAWKKVE

hS 315 RIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMQ.RVGQRGSGLSMS  
mS 316 RIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMQ.RVGQRGSGLSMS  
hN 324 RIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMQ.RVGQRGSGLSMS  
mN 324 RIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMQ.RVGQRGSGLSMS

hS 364 PARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMEDADQORIKFINMNG  
mS 366 PARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMEDADQORIKFINMNG  
hN 373 PARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMEDADQORIKFINMNG  
mN 373 PARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMEDADQORIKFINMNG

hS 414 LMADPMKVYKDRQVMN  
mS 415 LMADPMKVYKDRQVMN  
hN 423 LMADPMKVYKDRQVMN  
mN 423 LMADPMKVYKDRQVMN

SANT "A"

hSMRte-A 430 MWSEQEKETFREKFMHPKNFGLIASFLERKTVAECVLYYYLTCKKNENYKSLVRRSY  
mSMRte-A 431 MWSEQEKETFREKFMHPKNFGLIASFLERKTVAECVLYYYLTCKKNENYKSLVRRSY  
hNCoR-A 439 MWSEQEKETFREKFMHPKNFGLIASFLERKTVAECVLYYYLTCKKNENYKSLVRRSY  
mNCoR-A 439 MWSEQEKETFREKFMHPKNFGLIASFLERKTVAECVLYYYLTCKKNENYKSLVRRSY  
hSMRte-B 613 RWTEEEEMETAKKGLLEHGRNWSAIAARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK

Myb Signatures: WSxxEDxxxx WxxIAxxxxxxRxxxxxxxxWxxx  
Myb Structure: hhhhhhhhhhhhhh hhhhhh hhhhhhhhhh

hSMRte-B 613 RWTEEEEMETAKKGLLEHGRNWSAIAARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK  
mSMRte-B 610 RWTEEEEMETAKKGLLEHGRNWSAIAARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK  
hNCoR-B 613 RWTEEEEMETAKKGLLEHGRNWSAIAARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK  
mNCoR-B 622 RWTEEEEMETAKKGLLEHGRNWSAIAARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK  
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SANT "B"

Fig. 5

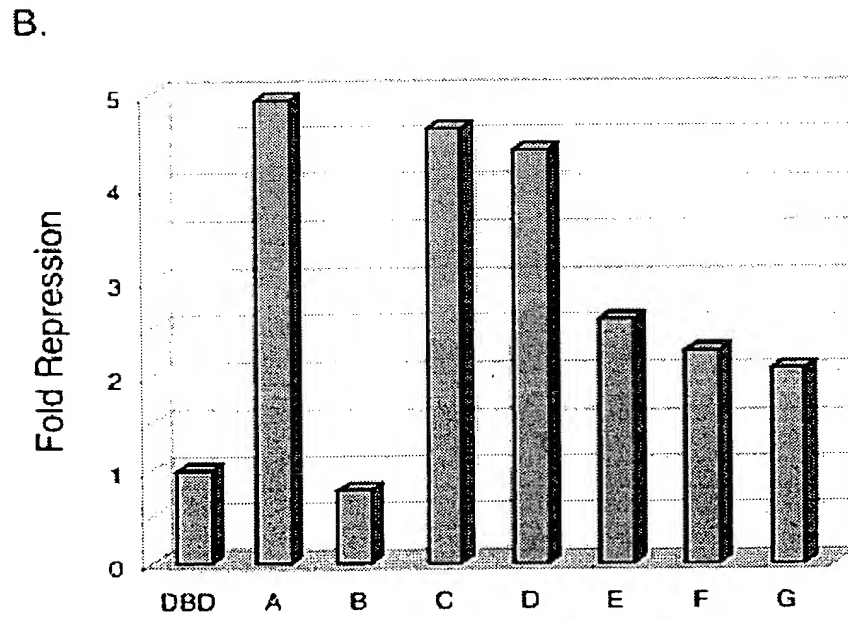
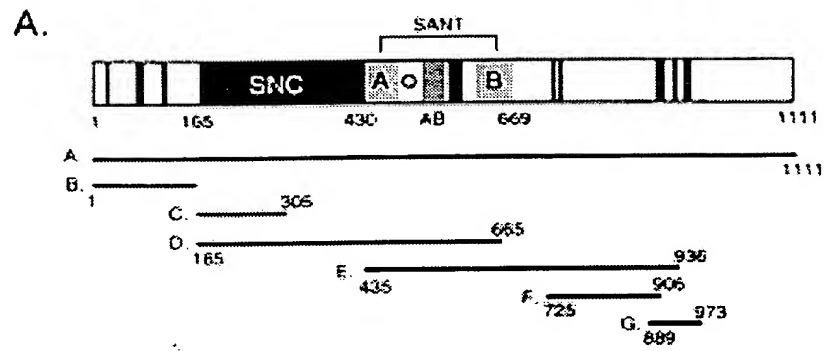
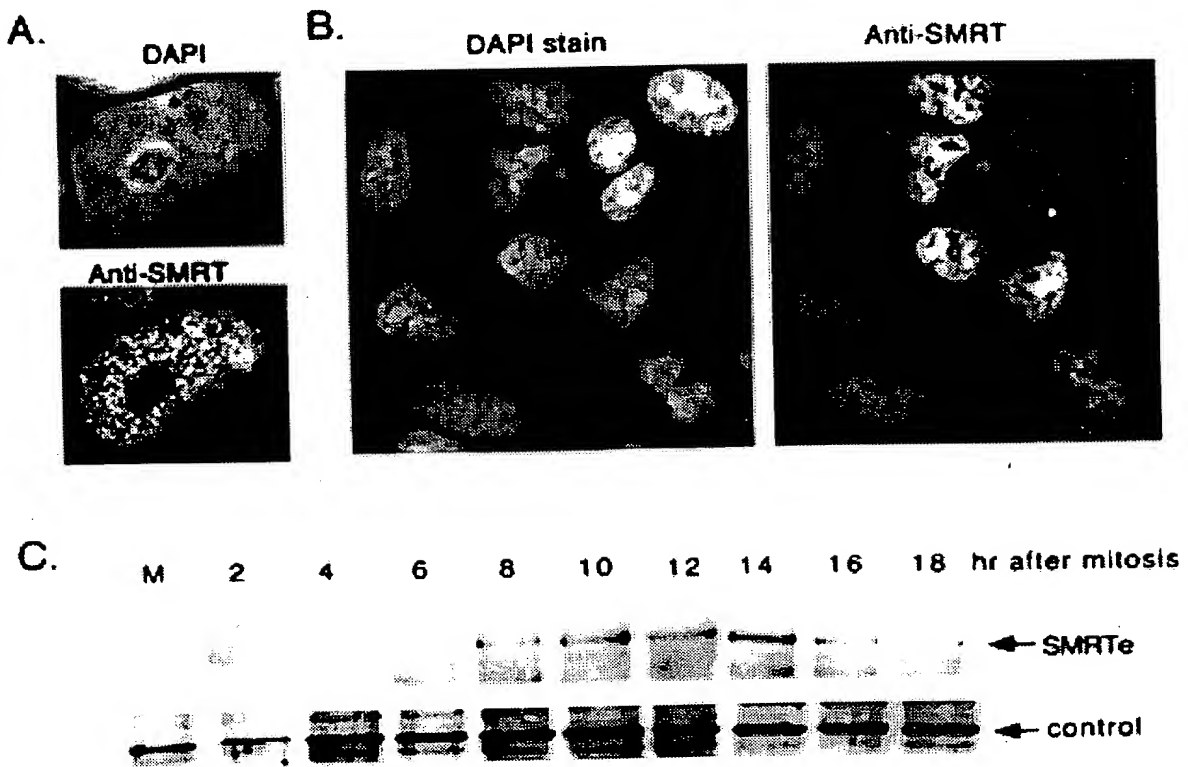


Fig. 6



### E13.5

